

LWS  
A12

SEQUENCE LISTING

<110> Soto, Ana, et al.

<120> A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION AND USES THEREOF

<130> MBI-008-1

<140>

<141>

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 5271

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66)..(4238)

<400> 1

ccggagagcc ccggagttag cggagttagc agtcggcaag ccggaggggt agaaatattt 60

ctgtc atg gct cat tca aag act agg acc aat gat gga aaa att aca tat 110

Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr  
1 5 10 15

ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158

Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met  
20 25 30

gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206

Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln  
35 40 45

gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tca cat ctt 254

Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu  
50 55 60

gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta atg 302

Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu  
65 70 75

gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350

Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala  
80 85 90 95

cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398

Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr  
100 105 110

aga cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg 446

Arg Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg  
115 120 125

tat ttt tat tta ctt gag aac att gct tgg gtc aag tca tat aac ata 494

Tyr Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile  
130 135 140

ccggagagcc ccggagttag cggagttagc agtcggcaag ccggaggggt agaaatattt 60

tgc ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga	542
Cys Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg	
145 150 155	
acc tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg	590
Thr Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met	
160 165 170 175	
cac atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg	638
His Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val	
180 185 190	
tct cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat	686
Ser Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His	
195 200 205	
aag aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag	734
Lys Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys	
210 215 220	
agg aca gct caa gct att gag cca tat att acc act ttt ttt aat cag	782
Arg Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln	
225 230 235	
gtt ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc	830
Val Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val	
240 245 250 255	
ttt gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc	878
Phe Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu	
260 265 270	
tct gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag	926
Ser Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu	
275 280 285	
gag cgc cta caa gtt gtt aaa cta ctg gca aaa atg ttt ggg gca aag	974
Glu Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys	
290 295 300	
gat tca gaa ttg gct tct caa aac aag cca ctt tgg cag tgc tac ttg	1022
Asp Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu	
305 310 315	
ggc agg ttt aat gat atc cat gta cca atc cgc ctg gaa tgt gtg aaa	1070
Gly Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys	
320 325 330 335	
ttt gct agc cat tgt ctc atg aac cat cct gat tta gca aaa gac tta	1118
Phe Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu	
340 345 350	
aca gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga	1166
Thr Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg	
355 360 365	
cat gat gtt att gtg tca ata gtt aca gct gct aaa aag gat att ctt	1214
His Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu	
370 375 380	
ctg gtc aat gat cac tta ctt aat ttt gtg aga gag aga aca tta gac	1262
Leu Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp	
385 390 395	

aaa cga tgg aga gta cgc aaa gaa gcc atg atg gga ctt gcc caa att	1310
Lys Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Ile	
400 405 410 415	
tat aag aaa tat gct tta cag tca gca gct gga aaa gat gct gca aaa	1358
Tyr Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys	
420 425 430	
cag ata gca tgg atc aaa gac aaa ttg cta cat ata tat tat caa aat	1406
Gln Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn	
435 440 445	
agt att gat gat cga cta ctt gtt gaa cgg atc ttt gct caa tac atg	1454
Ser Ile Asp Asp Arg Leu Leu Val Glu Arg Ile Phe Ala Gln Tyr Met	
450 455 460	
gtt cct cac aat tta gaa act aca gaa cgg atg aaa tgc tta tat tac	1502
Val Pro His Asn Leu Glu Thr Thr Glu Arg Met Lys Cys Leu Tyr Tyr	
465 470 475	
ttg tat gcc aca ctg gat tta aat gct gtg aaa gca ttg aat gaa atg	1550
Leu Tyr Ala Thr Leu Asp Leu Asn Ala Val Lys Ala Leu Asn Glu Met	
480 485 490 495	
tgg aaa tgt caa aat ctg ctc cga cat caa gta aag gat ttg ctt gac	1598
Trp Lys Cys Gln Asn Leu Leu Arg His Gln Val Lys Asp Leu Leu Asp	
500 505 510	
ttg att aag caa ccc aaa aca gat gcc agt gtc aag gcc ata ttt tca	1646
Leu Ile Lys Gln Pro Lys Thr Asp Ala Ser Val Lys Ala Ile Phe Ser	
515 520 525	
aaa gtg atg gtt att aca aga aat tta cct gat cct ggt aag gct cag	1694
Lys Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln	
530 535 540	
gat ttc atg aag aaa ttc aca cag gtg tta gaa gat gat gag aaa ata	1742
Asp Phe Met Lys Lys Phe Thr Gln Val Leu Glu Asp Asp Glu Lys Ile	
545 550 555	
aga aag cag tta gaa gta ctt gtt agt cca aca tgc tcc tgc aag cag	1790
Arg Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln	
560 565 570 575	
gct gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa	1838
Ala Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys	
580 585 590	
cag cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg	1886
Gln Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg	
595 600 605	
ata gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa	1934
Ile Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys	
610 615 620	
caa gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt	1982
Gln Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly	
625 630 635	
gtt cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta	2030
Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val	
640 645 650 655	

ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa	2078
Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu	
660 665 670	
tca tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct	2126
Ser Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala	
675 680 685	
gca cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt	2174
Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe	
690 695 700	
cca cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa	2222
Pro His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys	
705 710 715	
aaa gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg	2270
Lys Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala	
720 725 730 735	
ata ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg	2318
Ile Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu	
740 745 750	
cat aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg	2366
His Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu	
755 760 765	
gtt act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct	2414
Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala	
770 775 780	
cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg	2462
Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met	
785 790 795	
aat gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat	2510
Asn Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp	
800 805 810 815	
gaa gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg	2558
Glu Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met	
820 825 830	
atg gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga	2606
Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly	
835 840 845	
act tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac	2654
Thr Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp	
850 855 860	
ttg aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga	2702
Leu Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg	
865 870 875	
ctt gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac	2750
Leu Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr	
880 885 890 895	
cat gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc	2798
His Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile	
900 905 910	

aac gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac	2846
Asn Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His	
915 920 925	
aaa ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt	2894
Lys Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys	
930 935 940	
gcc ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg	2942
Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg	
945 950 955	
caa tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag	2990
Gln Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln	
960 965 970 975	
cat gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt	3038
His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val	
980 985 990	
gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa	3086
Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys	
995 1000 1005	
gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt	3134
Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe	
1010 1015 1020	
gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt	3182
Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe	
1025 1030 1035	
atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga	3230
Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly	
1040 1045 1050 1055	
cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt	3278
Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val	
1060 1065 1070	
gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct	3326
Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser	
1075 1080 1085	
cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag	3374
Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys	
1090 1095 1100	
aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt	3422
Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe	
1105 1110 1115	
ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac	3470
Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn	
1120 1125 1130 1135	
aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga	3518
Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg	
1140 1145 1150	
atg gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct	3566
Met Glu Thr Val Ser Asn Ala Ser Ser Ser Ser Asn Pro Ser Ser Pro	
1155 1160 1165	

gga aga ata aag ggg agg ctt gat agt tct gaa atg gat cac agt gaa 3614  
 Gly Arg Ile Lys Gly Arg Leu Asp Ser Ser Glu Met Asp His Ser Glu  
 1170 1175 1180  
  
 aat gaa gat tac aca atg tct tca cct ttg ccg ggg aaa aaa agt gac 3662  
 Asn Glu Asp Tyr Thr Met Ser Ser Pro Leu Pro Gly Lys Lys Ser Asp  
 1185 1190 1195  
  
 aag aga gac gac tct gat ctt gta agg tct gaa ttg gag aag cct aga 3710  
 Lys Arg Asp Asp Ser Asp Leu Val Arg Ser Glu Leu Glu Lys Pro Arg  
 1200 1205 1210 1215  
  
 ggc agg aaa aaa acg ccc gtc aca gaa cag gag gag aaa tta ggt atg 3758  
 Gly Arg Lys Lys Thr Pro Val Thr Glu Gln Glu Glu Lys Leu Gly Met  
 1220 1225 1230  
  
 gat gac ttg act aag ttg gta cag gaa cag aaa cct aaa ggc agt cag 3806  
 Asp Asp Leu Thr Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gln  
 1235 1240 1245  
  
 cga agt cgg aaa aga ggc cat acg gct tca gaa tct gat gaa cag cag 3854  
 Arg Ser Arg Lys Arg Gly His Thr Ala Ser Glu Ser Asp Glu Gln Gln  
 1250 1255 1260  
  
 tgg cct gag gaa aag agg ctc aaa gaa gat ata tta gaa aat gaa gat 3902  
 Trp Pro Glu Glu Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp  
 1265 1270 1275  
  
 gaa cag aat agt ccg cca aaa aag ggt aaa aga ggc cga cca cca aaa 3950  
 Glu Gln Asn Ser Pro Pro Lys Lys Gly Lys Arg Gly Arg Pro Pro Lys  
 1280 1285 1290 1295  
  
 cct ctt ggt gga ggt aca cca aaa gaa gag cca aca atg aaa act tct 3998  
 Pro Leu Gly Gly Gly Thr Pro Lys Glu Glu Pro Thr Met Lys Thr Ser  
 1300 1305 1310  
  
 aaa aaa gga agc aaa aaa aaa tct gga cct cca gca cca gag gag gag 4046  
 Lys Lys Gly Ser Lys Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu  
 1315 1320 1325  
  
 gaa gaa gaa gaa aga caa agt gga aat acg gaa cag aag tcc aaa agc 4094  
 Glu Glu Glu Glu Arg Gln Ser Gly Asn Thr Glu Gln Lys Ser Lys Ser  
 1330 1335 1340  
  
 aaa cag cac cga gtg tca agg aga gca cag cag aga gca gaa tct cct 4142  
 Lys Gln His Arg Val Ser Arg Arg Ala Gln Gln Arg Ala Glu Ser Pro  
 1345 1350 1355  
  
 gaa tct agt gca att gaa tcc aca cag tcc aca cca cag aaa gga cga 4190  
 Glu Ser Ser Ala Ile Glu Ser Thr Gln Ser Thr Pro Gln Lys Gly Arg  
 1360 1365 1370 1375  
  
 gga aga cca tca aaa acg cca tca cca tca caa cca aaa aaa aat gtg 4238  
 Gly Arg Pro Ser Lys Thr Pro Ser Pro Ser Gln Pro Lys Lys Asn Val  
 1380 1385 1390  
  
 taagttgtaa atattacatt tcaaaccaat ttcaaattat tttgcaaaag ttcctaaatt 4298  
 tgtaaacata catattgctg tattttaatt ccatatattt agccccatta cactaggtac 4358  
 ggcggcgaag tgctaaaagg gaacggcgat gaacaaatgt aattaataac tttctctgtg 4418  
 aaagcttttg aaaaatcttt tttttttttt tttttttttg gtcaagcttg aggctgaata 4478

aagcctttga tgcacaaaat gggactgctg aagagtggac agttggacct tactttggtg 4538  
accccataca tttgtggtca catgcttttag ccatacacat ggtaacattg actatggagt 4598  
cttgtgaaag tgtaatgtgc gatggctatg tagacataaa gaagaaactt gtaaataatct 4658  
tttttctttt ttttaatgtt tctgatttct gaagtgttg tatagctttt atctgcggt 4718  
ttaaactgac agtaccgcac tgtttattgg atctattgat ttgaaaagaa tttgttagga 4778  
tagatcttaa gcagtaatct gtcagtgttt gtatttgtat tttctgcaat tttactgtga 4838  
aaaaaaattt gttttcaaca attggtgtca ttttcttgat gtcactattt gttggagagt 4898  
taaagtgtct cttccctttg tgtatcttac ctagtgttta ctccctgggca cccttaatct 4958  
tcagaggtgc taaattgtct gccattacac cagaaggatg cctctgatag gaggacaacc 5018  
atgcaaattg tgaaatagtc ctgaagtctt tggattactt tacacctcag tattgatttg 5078  
tcccagaatt ttctggcctt tcattggcaat gaaaatttta agaagaaaga tttaaagtat 5138  
tttaatttta aagagtgtgt tataaaataa tgtactgaat tctttatccc attttatcat 5198  
cctttcagtt tttattaatc tactgtatca ataaaattct gtaatttgaa tgagtaaaaa 5258  
aaaaaaaaaaa aaa 5271

<210> 2  
<211> 1391  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro  
1 5 10 15  
Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val  
20 25 30  
Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp  
35 40 45  
Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala  
50 55 60  
Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu Val  
65 70 75 80  
Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro  
85 90 95  
Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr Arg  
100 105 110  
Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg Tyr  
115 120 125  
Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile Cys  
130 135 140  
Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg Thr

145		150		155		160
Leu Phe Ser Val	Ile Asn Asn Gly His	Asn Gln Lys Val	His Met His			
	165	170	175			
Met Val Asp	Leu Met Ser Ser	Ile Ile Cys Glu Gly	Asp Thr Val Ser			
	180	185	190			
Gln Glu	Leu Leu Asp Thr	Val Leu Val Asn Leu	Val Pro Ala His Lys			
	195	200	205			
Asn Leu Asn	Lys Gln Ala Tyr	Asp Leu Ala Lys	Ala Leu Leu Lys Arg			
	210	215	220			
Thr Ala Gln	Ala Ile Glu Pro Tyr	Ile Thr Thr Phe Phe	Asn Gln Val			
225	230	235	240			
Leu Met Leu	Gly Lys Thr Ser	Ile Ser Asp Leu Ser	Glu His Val Phe			
	245	250	255			
Asp Leu Ile	Leu Glu Leu Tyr	Asn Ile Asp Ser	His Leu Leu Ser			
	260	265	270			
Val Leu Pro	Gln Leu Glu Phe	Lys Leu Lys Ser	Asn Asp Asn Glu Glu			
	275	280	285			
Arg Leu Gln	Val Val Lys Leu Leu	Ala Lys Met Phe Gly	Ala Lys Asp			
	290	295	300			
Ser Glu Leu	Ala Ser Gln Asn	Lys Pro Leu Trp	Gln Cys Tyr Leu Gly			
305	310	315	320			
Arg Phe Asn	Asp Ile His Val	Pro Ile Arg Leu	Glu Cys Val Lys Phe			
	325	330	335			
Ala Ser His	Cys Leu Met Asn	His Pro Asp Leu	Ala Lys Asp Leu Thr			
	340	345	350			
Glu Tyr Leu	Lys Val Arg Ser	His Asp Pro Glu	Glu Ala Ile Arg His			
	355	360	365			
Asp Val Ile	Val Ser Ile Val	Thr Ala Ala Lys	Lys Asp Ile Leu Leu			
	370	375	380			
Val Asn Asp	His Leu Leu Asn	Phe Val Arg Glu	Arg Thr Leu Asp Lys			
385	390	395	400			
Arg Trp Arg	Val Arg Lys Glu	Ala Met Met Gly	Leu Ala Gln Ile Tyr			
	405	410	415			
Lys Lys Tyr	Ala Leu Gln Ser	Ala Ala Gly Lys	Asp Ala Ala Lys Gln			
	420	425	430			
Ile Ala Trp	Ile Lys Asp Lys	Leu Leu His Ile	Tyr Tyr Gln Asn Ser			
	435	440	445			
Ile Asp Asp	Arg Leu Leu Val	Glu Arg Ile Phe	Ala Gln Tyr Met Val			
	450	455	460			
Pro His Asn	Leu Glu Thr Thr	Glu Arg Met Lys	Cys Leu Tyr Tyr Leu			
465	470	475	480			
Tyr Ala Thr	Leu Asp Leu Asn	Ala Val Lys Ala	Leu Asn Glu Met Trp			
	485	490	495			



Lys Cys Gln Asn Leu Leu Arg His Gln Val Lys Asp Leu Leu Asp Leu  
 500 505 510  
 Ile Lys Gln Pro Lys Thr Asp Ala Ser Val Lys Ala Ile Phe Ser Lys  
 515 520 525  
 Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln Asp  
 530 535 540  
 Phe Met Lys Lys Phe Thr Gln Val Leu Glu Asp Asp Glu Lys Ile Arg  
 545 550 555 560  
 Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln Ala  
 565 570 575  
 Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys Gln  
 580 585 590  
 Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg Ile  
 595 600 605  
 Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys Gln  
 610 615 620  
 Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly Val  
 625 630 635 640  
 Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val Leu  
 645 650 655  
 Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu Ser  
 660 665 670  
 Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala Ala  
 675 680 685  
 Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe Pro  
 690 695 700  
 His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys Lys  
 705 710 715 720  
 Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala Ile  
 725 730 735  
 Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu His  
 740 745 750  
 Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu Val  
 755 760 765  
 Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala Pro  
 770 775 780  
 Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met Asn  
 785 790 795 800  
 Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp Glu  
 805 810 815  
 Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met Met  
 820 825 830

Val	Arg	Trp	Leu	Leu	Gly	Met	Lys	Asn	Asn	His	Ser	Lys	Ser	Gly	Thr	835	840	845
Ser	Thr	Leu	Arg	Leu	Leu	Thr	Thr	Ile	Leu	His	Ser	Asp	Gly	Asp	Leu	850	855	860
Thr	Glu	Gln	Gly	Lys	Ile	Ser	Lys	Pro	Asp	Met	Ser	Arg	Leu	Arg	Leu	865	870	875
Ala	Ala	Gly	Ser	Ala	Ile	Val	Lys	Leu	Ala	Gln	Glu	Pro	Cys	Tyr	His	885	890	895
Glu	Ile	Ile	Thr	Leu	Glu	Gln	Tyr	Gln	Leu	Cys	Ala	Leu	Ala	Ile	Asn	900	905	910
Asp	Glu	Cys	Tyr	Gln	Val	Arg	Gln	Val	Phe	Ala	Gln	Lys	Leu	His	Lys	915	920	925
Gly	Leu	Ser	Arg	Leu	Arg	Leu	Pro	Leu	Glu	Tyr	Met	Ala	Ile	Cys	Ala	930	935	940
Leu	Cys	Ala	Lys	Asp	Pro	Val	Lys	Glu	Arg	Arg	Ala	His	Ala	Arg	Gln	945	950	955
Cys	Leu	Val	Lys	Asn	Ile	Asn	Val	Arg	Arg	Glu	Tyr	Leu	Lys	Gln	His	965	970	975
Ala	Ala	Val	Ser	Glu	Lys	Leu	Leu	Ser	Leu	Leu	Pro	Glu	Tyr	Val	Val	980	985	990
Pro	Tyr	Thr	Ile	His	Leu	Leu	Ala	His	Asp	Pro	Asp	Tyr	Val	Lys	Val	995	1000	1005
Gln	Asp	Ile	Glu	Gln	Leu	Lys	Asp	Val	Lys	Glu	Cys	Leu	Trp	Phe	Val	1010	1015	1020
Leu	Glu	Ile	Leu	Met	Ala	Lys	Asn	Glu	Asn	Asn	Ser	His	Ala	Phe	Ile	1025	1030	1035
Arg	Lys	Met	Val	Glu	Asn	Ile	Lys	Gln	Thr	Lys	Asp	Ala	Gln	Gly	Pro	1045	1050	1055
Asp	Asp	Ala	Lys	Met	Asn	Glu	Lys	Leu	Tyr	Thr	Val	Cys	Asp	Val	Ala	1060	1065	1070
Met	Asn	Ile	Ile	Met	Ser	Lys	Ser	Thr	Thr	Tyr	Ser	Leu	Glu	Ser	Pro	1075	1080	1085
Lys	Asp	Pro	Val	Leu	Pro	Ala	Arg	Phe	Phe	Thr	Gln	Pro	Asp	Lys	Asn	1090	1095	1100
Phe	Ser	Asn	Thr	Lys	Asn	Tyr	Leu	Pro	Pro	Glu	Met	Lys	Ser	Phe	Phe	1105	1110	1115
Thr	Pro	Gly	Lys	Pro	Lys	Thr	Thr	Asn	Val	Leu	Gly	Ala	Val	Asn	Lys	1125	1130	1135
Pro	Leu	Ser	Ser	Ala	Gly	Lys	Gln	Ser	Gln	Thr	Lys	Ser	Ser	Arg	Met	1140	1145	1150
Glu	Thr	Val	Ser	Asn	Ala	Ser	Ser	Ser	Asn	Pro	Ser	Ser	Pro	Gly		1155	1160	1165
Arg	Ile	Lys	Gly	Arg	Leu	Asp	Ser	Ser	Glu	Met	Asp	His	Ser	Glu	Asn			

```

1170              1175              1180
Glu Asp Tyr Thr Met Ser Ser Pro Leu Pro Gly Lys Lys Ser Asp Lys
185              1190              1195              120
Arg Asp Asp Ser Asp Leu Val Arg Ser Glu Leu Glu Lys Pro Arg Gly
              1205              1210              1215
Arg Lys Lys Thr Pro Val Thr Glu Gln Glu Glu Lys Leu Gly Met Asp
              1220              1225              1230
Asp Leu Thr Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gln Arg
              1235              1240              1245
Ser Arg Lys Arg Gly His Thr Ala Ser Glu Ser Asp Glu Gln Gln Trp
              1250              1255              1260
Pro Glu Glu Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp Glu
265              1270              1275              128
Gln Asn Ser Pro Pro Lys Lys Gly Lys Arg Gly Arg Pro Pro Lys Pro
              1285              1290              1295
Leu Gly Gly Gly Thr Pro Lys Glu Glu Pro Thr Met Lys Thr Ser Lys
              1300              1305              1310
Lys Gly Ser Lys Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu Glu
              1315              1320              1325
Glu Glu Glu Arg Gln Ser Gly Asn Thr Glu Gln Lys Ser Lys Ser Lys
              1330              1335              1340
Gln His Arg Val Ser Arg Arg Ala Gln Gln Arg Ala Glu Ser Pro Glu
345              1350              1355              136
Ser Ser Ala Ile Glu Ser Thr Gln Ser Thr Pro Gln Lys Gly Arg Gly
              1365              1370              1375
Arg Pro Ser Lys Thr Pro Ser Pro Ser Gln Pro Lys Lys Asn Val
              1380              1385              1390

```

```

<210> 3
<211> 4173
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(4173)

```

```

<400> 3
atg gct cat tca aag act agg acc aat gat gga aaa att aca tat ccg 48
Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro
  1              5              10              15

cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg gtg 96
Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val
              20              25              30

aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag gac 144
Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp
              35              40              45

```

tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt gct	192
Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala	
50 55 60	
tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg gta	240
Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu Val	
65 70 75 80	
gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct cct	288
Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro	
85 90 95	
tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca aga	336
Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr Arg	
100 105 110	
cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg tat	384
Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg Tyr	
115 120 125	
ttt tat tta ctt gag aac att gct tgg gtc aag tca tat aac ata tgc	432
Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile Cys	
130 135 140	
ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga acc	480
Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg Thr	
145 150 155 160	
tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg cac	528
Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met His	
165 170 175	
atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg tct	576
Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val Ser	
180 185 190	
cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat aag	624
Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His Lys	
195 200 205	
aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag agg	672
Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys Arg	
210 215 220	
aca gct caa gct att gag cca tat att acc act ttt ttt aat cag gtt	720
Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln Val	
225 230 235 240	
ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc ttt	768
Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val Phe	
245 250 255	
gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc tct	816
Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu Ser	
260 265 270	
gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag gag	864
Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu Glu	
275 280 285	
cgc cta caa gtt gtt aaa cta ctg gca aaa atg ttt ggg gca aag gat	912
Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys Asp	
290 295 300	



aag cag tta gaa gta ctt gtt agt cca aca tgc tcc tgc aag cag gct	1728
Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln Ala	
565 570 575	
gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa cag	1776
Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys Gln	
580 585 590	
cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg ata	1824
Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg Ile	
595 600 605	
gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa caa	1872
Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys Gln	
610 615 620	
gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt gtt	1920
Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly Val	
625 630 635 640	
cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta ctc	1968
Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val Leu	
645 650 655	
tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa tca	2016
Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu Ser	
660 665 670	
tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct gca	2064
Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala Ala	
675 680 685	
cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt cca	2112
Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe Pro	
690 695 700	
cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa aaa	2160
His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys Lys	
705 710 715 720	
gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg ata	2208
Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala Ile	
725 730 735	
ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg cat	2256
Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu His	
740 745 750	
aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg gtt	2304
Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu Val	
755 760 765	
act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct cct	2352
Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala Pro	
770 775 780	
tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg aat	2400
Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met Asn	
785 790 795 800	
gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat gaa	2448
Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp Glu	
805 810 815	

gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg atg	2496
Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met Met	
820 825 830	
gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga act	2544
Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly Thr	
835 840 845	
tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac ttg	2592
Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp Leu	
850 855 860	
aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga ctt	2640
Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg Leu	
865 870 875 880	
gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac cat	2688
Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr His	
885 890 895	
gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc aac	2736
Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile Asn	
900 905 910	
gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac aaa	2784
Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His Lys	
915 920 925	
ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt gcc	2832
Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys Ala	
930 935 940	
ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg caa	2880
Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg Gln	
945 950 955 960	
tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag cat	2928
Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln His	
965 970 975	
gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt gtt	2976
Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val Val	
980 985 990	
cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa gta	3024
Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys Val	
995 1000 1005	
cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt gtt	3072
Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe Val	
1010 1015 1020	
ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt atc	3120
Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe Ile	
1025 1030 1035 1040	
aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga cca	3168
Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly Pro	
1045 1050 1055	
gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt gcc	3216
Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val Ala	
1060 1065 1070	

atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct cct	3264
Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser Pro	
1075 1080 1085	
aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag aat	3312
Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys Asn	
1090 1095 1100	
ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt ttc	3360
Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe Phe	
1105 1110 1115 1120	
act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac aag	3408
Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn Lys	
1125 1130 1135	
cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga atg	3456
Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg Met	
1140 1145 1150	
gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct gga	3504
Glu Thr Val Ser Asn Ala Ser Ser Ser Ser Asn Pro Ser Ser Pro Gly	
1155 1160 1165	
aga ata aag ggg agg ctt gat agt tct gaa atg gat cac agt gaa aat	3552
Arg Ile Lys Gly Arg Leu Asp Ser Ser Glu Met Asp His Ser Glu Asn	
1170 1175 1180	
gaa gat tac aca atg tct tca cct ttg ccg ggg aaa aaa agt gac aag	3600
Glu Asp Tyr Thr Met Ser Ser Pro Leu Pro Gly Lys Lys Ser Asp Lys	
1185 1190 1195 1200	
aga gac gac tct gat ctt gta agg tct gaa ttg gag aag cct aga ggc	3648
Arg Asp Asp Ser Asp Leu Val Arg Ser Glu Leu Glu Lys Pro Arg Gly	
1205 1210 1215	
agg aaa aaa acg ccc gtc aca gaa cag gag gag aaa tta ggt atg gat	3696
Arg Lys Lys Thr Pro Val Thr Glu Gln Glu Glu Lys Leu Gly Met Asp	
1220 1225 1230	
gac ttg act aag ttg gta cag gaa cag aaa cct aaa ggc agt cag cga	3744
Asp Leu Thr Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gln Arg	
1235 1240 1245	
agt cgg aaa aga ggc cat acg gct tca gaa tct gat gaa cag cag tgg	3792
Ser Arg Lys Arg Gly His Thr Ala Ser Glu Ser Asp Glu Gln Gln Trp	
1250 1255 1260	
cct gag gaa aag agg ctc aaa gaa gat ata tta gaa aat gaa gat gaa	3840
Pro Glu Glu Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp Glu	
1265 1270 1275 1280	
cag aat agt ccg cca aaa aag ggt aaa aga ggc cga cca cca aaa cct	3888
Gln Asn Ser Pro Pro Lys Lys Gly Lys Arg Gly Arg Pro Pro Lys Pro	
1285 1290 1295	
ctt ggt gga ggt aca cca aaa gaa gag cca aca atg aaa act tct aaa	3936
Leu Gly Gly Gly Thr Pro Lys Glu Glu Pro Thr Met Lys Thr Ser Lys	
1300 1305 1310	
aaa gga agc aaa aaa aaa tct gga cct cca gca cca gag gag gag gaa	3984
Lys Gly Ser Lys Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu Glu	
1315 1320 1325	



gaa gaa gaa aga caa agt gga aat acg gaa cag aag tcc aaa agc aaa 4032  
 Glu Glu Glu Arg Gln Ser Gly Asn Thr Glu Gln Lys Ser Lys Ser Lys  
 1330 1335 1340

cag cac cga gtg tca agg aga gca cag cag aga gca gaa tct cct gaa 4080  
 Gln His Arg Val Ser Arg Arg Ala Gln Gln Arg Ala Glu Ser Pro Glu  
 1345 1350 1355 1360

tct agt gca att gaa tcc aca cag tcc aca cca cag aaa gga cga gga 4128  
 Ser Ser Ala Ile Glu Ser Thr Gln Ser Thr Pro Gln Lys Gly Arg Gly  
 1365 1370 1375

aga cca tca aaa acg cca tca cca tca caa cca aaa aaa aat gtg 4173  
 Arg Pro Ser Lys Thr Pro Ser Pro Ser Gln Pro Lys Lys Asn Val  
 1380 1385 1390

<210> 4  
 <211> 5355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (150)..(4322)

<400> 4  
 cggagaggag gaggaacggc agggctggct gcggaagggg aggggggggg agaaggcgat 60  
 tggatgcggc ggcggcggcg gatcccgag agccccggag tgagcggagt agcgagtcgg 120  
 caaccggag gggtagaaat atttctgtc atg gct cat tca aag act agg acc 173  
 Met Ala His Ser Lys Thr Arg Thr  
 1 5

aat gat gga aaa att aca tat ccg cct ggg gtc aag gaa ata tca gat 221  
 Asn Asp Gly Lys Ile Thr Tyr Pro Pro Gly Val Lys Glu Ile Ser Asp  
 10 15 20

aaa ata tct aaa gag gag atg gtg aga cga tta aag atg gtt gtg aaa 269  
 Lys Ile Ser Lys Glu Glu Met Val Arg Arg Leu Lys Met Val Val Lys  
 25 30 35 40

act ttt atg gat atg gac cag gac tct gaa gaa gaa aag gag ctt tat 317  
 Thr Phe Met Asp Met Asp Gln Asp Ser Glu Glu Glu Lys Glu Leu Tyr  
 45 50 55

tta aac cta gct tta cat ctt gct tca gat ttt ttt ctc aag cat cct 365  
 Leu Asn Leu Ala Leu His Leu Ala Ser Asp Phe Phe Leu Lys His Pro  
 60 65 70

ggt aaa gat gtt cgc tta ctg gta gcc tgc tgc ctt gct gat att ttc 413  
 Gly Lys Asp Val Arg Leu Leu Val Ala Cys Cys Leu Ala Asp Ile Phe  
 75 80 85

agg att tat gct cct gaa gct cct tac aca tcc cct gat aaa cta aag 461  
 Arg Ile Tyr Ala Pro Glu Ala Pro Tyr Thr Ser Pro Asp Lys Leu Lys  
 90 95 100

gat ata ttt atg ttt ata aca aga cag ttg aag ggg cta gag gat aca 509  
 Asp Ile Phe Met Phe Ile Thr Arg Gln Leu Lys Gly Leu Glu Asp Thr  
 105 110 115 120

aag agc cca caa ttc aat agg tat ttt tat tta ctt gag aac att gct 557

Lys	Ser	Pro	Gln	Phe	Asn	Arg	Tyr	Phe	Tyr	Leu	Leu	Glu	Asn	Ile	Ala		
				125					130					135			
tgg	gtc	aag	tca	tat	aac	ata	tgc	ttt	gag	tta	gaa	gat	agc	aat	gaa	605	
Trp	Val	Lys	Ser	Tyr	Asn	Ile	Cys	Phe	Glu	Leu	Glu	Asp	Ser	Asn	Glu		
			140					145					150				
att	ttc	acc	cag	cta	tac	aga	acc	tta	ttt	tca	gtt	ata	aac	aat	ggc	653	
Ile	Phe	Thr	Gln	Leu	Tyr	Arg	Thr	Leu	Phe	Ser	Val	Ile	Asn	Asn	Gly		
		155					160					165					
cac	aat	cag	aaa	gtc	cat	atg	cac	atg	gta	gac	ctt	atg	agc	tct	att	701	
His	Asn	Gln	Lys	Val	His	Met	His	Met	Val	Asp	Leu	Met	Ser	Ser	Ile		
	170					175					180						
att	tgt	gaa	ggc	gat	aca	gtg	tct	cag	gag	ctt	ttg	gat	acg	gtt	tta	749	
Ile	Cys	Glu	Gly	Asp	Thr	Val	Ser	Gln	Glu	Leu	Leu	Asp	Thr	Val	Leu		
185					190					195					200		
gta	aat	ctg	gta	cct	gct	cat	aag	aat	tta	aac	aag	caa	gca	tat	gat	797	
Val	Asn	Leu	Val	Pro	Ala	His	Lys	Asn	Leu	Asn	Lys	Gln	Ala	Tyr	Asp		
			205					210					215				
ttg	gca	aag	gct	tta	ctg	aag	agg	aca	gct	caa	gct	att	gag	cca	tat	845	
Leu	Ala	Lys	Ala	Leu	Leu	Lys	Arg	Thr	Ala	Gln	Ala	Ile	Glu	Pro	Tyr		
			220					225					230				
att	acc	act	ttt	ttt	aat	cag	gtt	ctg	atg	ctt	ggg	aaa	aca	tct	atc	893	
Ile	Thr	Thr	Phe	Phe	Asn	Gln	Val	Leu	Met	Leu	Gly	Lys	Thr	Ser	Ile		
		235				240						245					
agc	gat	ttg	tca	gag	cat	gtc	ttt	gac	tta	att	ttg	gag	ctc	tac	aat	941	
Ser	Asp	Leu	Ser	Glu	His	Val	Phe	Asp	Leu	Ile	Leu	Glu	Leu	Tyr	Asn		
	250					255					260						
att	gat	agt	cat	ttg	ctg	ctc	tct	gtt	tta	ccc	cag	ctt	gaa	ttt	aaa	989	
Ile	Asp	Ser	His	Leu	Leu	Leu	Ser	Val	Leu	Pro	Gln	Leu	Glu	Phe	Lys		
265				270					275					280			
tta	aag	agc	aat	gat	aat	gag	gag	cgc	cta	caa	gtt	gtt	aaa	cta	ctg	1037	
Leu	Lys	Ser	Asn	Asp	Asn	Glu	Glu	Arg	Leu	Gln	Val	Val	Lys	Leu	Leu		
			285					290					295				
gca	aaa	atg	ttt	ggg	gca	aag	gat	tca	gaa	ttg	gct	tct	caa	aac	aag	1085	
Ala	Lys	Met	Phe	Gly	Ala	Lys	Asp	Ser	Glu	Leu	Ala	Ser	Gln	Asn	Lys		
			300					305					310				
cca	ctt	tg	cag	tgc	tac	ttg	ggc	agg	ttt	aat	gat	atc	cat	gta	cca	1133	
Pro	Leu	Trp	Gln	Cys	Tyr	Leu	Gly	Arg	Phe	Asn	Asp	Ile	His	Val	Pro		
		315					320					325					
atc	cgc	ctg	gaa	tgt	gtg	aaa	ttt	gct	agc	cat	tgt	ctc	atg	aac	cat	1181	
Ile	Arg	Leu	Glu	Cys	Val	Lys	Phe	Ala	Ser	His	Cys	Leu	Met	Asn	His		
	330					335					340						
cct	gat	tta	gca	aaa	gac	tta	aca	gag	tat	ctt	aaa	gtg	agg	tca	cat	1229	
Pro	Asp	Leu	Ala	Lys	Asp	Leu	Thr	Glu	Tyr	Leu	Lys	Val	Arg	Ser	His		
345					350					355				360			
gac	cct	gag	gaa	gct	att	aga	cat	gat	gtt	att	gtg	tca	ata	gtt	aca	1277	
Asp	Pro	Glu	Glu	Ala	Ile	Arg	His	Asp	Val	Ile	Val	Ser	Ile	Val	Thr		
				365					370				375				
gct	gct	aaa	aag	gat	att	ctt	ctg	gtc	aat	gat	cac	tta	ctt	aat	ttt	1325	

Ala	Ala	Lys	Lys	Asp	Ile	Leu	Leu	Val	Asn	Asp	His	Leu	Leu	Asn	Phe		
			380					385					390				
gtg	aga	gag	aga	aca	tta	gac	aaa	cga	tgg	aga	gta	cgc	aaa	gaa	gcc	1373	
Val	Arg	Glu	Arg	Thr	Leu	Asp	Lys	Arg	Trp	Arg	Val	Arg	Lys	Glu	Ala		
			395				400					405					
atg	atg	gga	ctt	gcc	caa	att	tat	aag	aaa	tat	gct	tta	cag	tca	gca	1421	
Met	Met	Gly	Leu	Ala	Gln	Ile	Tyr	Lys	Lys	Tyr	Ala	Leu	Gln	Ser	Ala		
		410				415					420						
gct	gga	aaa	gat	gct	gca	aaa	cag	ata	gca	tgg	atc	aaa	gac	aaa	ttg	1469	
Ala	Gly	Lys	Asp	Ala	Ala	Lys	Gln	Ile	Ala	Trp	Ile	Lys	Asp	Lys	Leu		
425					430				435						440		
cta	cat	ata	tat	tat	caa	aat	agt	att	gat	gat	cga	cta	ctt	gtt	gaa	1517	
Leu	His	Ile	Tyr	Tyr	Gln	Asn	Ser	Ile	Asp	Asp	Arg	Leu	Leu	Val	Glu		
				445					450					455			
cgg	atc	ttt	gct	caa	tac	atg	gtt	cct	cac	aat	tta	gaa	act	aca	gaa	1565	
Arg	Ile	Phe	Ala	Gln	Tyr	Met	Val	Pro	His	Asn	Leu	Glu	Thr	Thr	Glu		
			460					465						470			
cgg	atg	aaa	tgc	tta	tat	tac	ttg	tat	gcc	aca	ctg	gat	tta	aat	gct	1613	
Arg	Met	Lys	Cys	Leu	Tyr	Tyr	Leu	Tyr	Ala	Thr	Leu	Asp	Leu	Asn	Ala		
		475					480					485					
gtg	aaa	gca	ttg	aat	gaa	atg	tgg	aaa	tgt	caa	aat	ctg	ctc	cga	cat	1661	
Val	Lys	Ala	Leu	Asn	Glu	Met	Trp	Lys	Cys	Gln	Asn	Leu	Leu	Arg	His		
		490				495					500						
caa	gta	aag	gat	ttg	ctt	gac	ttg	att	aag	caa	ccc	aaa	aca	gat	gcc	1709	
Gln	Val	Lys	Asp	Leu	Leu	Asp	Leu	Ile	Lys	Gln	Pro	Lys	Thr	Asp	Ala		
505					510					515					520		
agt	gtc	aag	gcc	ata	ttt	tca	aaa	gtg	atg	gtt	att	aca	aga	aat	tta	1757	
Ser	Val	Lys	Ala	Ile	Phe	Ser	Lys	Val	Met	Val	Ile	Thr	Arg	Asn	Leu		
				525					530					535			
cct	gat	cct	ggt	aag	gct	cag	gat	ttc	atg	aag	aaa	ttc	aca	cag	gtg	1805	
Pro	Asp	Pro	Gly	Lys	Ala	Gln	Asp	Phe	Met	Lys	Lys	Phe	Thr	Gln	Val		
			540					545					550				
tta	gaa	gat	gat	gag	aaa	ata	aga	aag	cag	tta	gaa	gta	ctt	gtt	agt	1853	
Leu	Glu	Asp	Asp	Glu	Lys	Ile	Arg	Lys	Gln	Leu	Glu	Val	Leu	Val	Ser		
			555				560					565					
cca	aca	tgc	tcc	tgc	aag	cag	gct	gaa	ggt	tgt	gtg	cgt	gaa	ata	act	1901	
Pro	Thr	Cys	Ser	Cys	Lys	Gln	Ala	Glu	Gly	Cys	Val	Arg	Glu	Ile	Thr		
		570				575					580						
aag	aag	ttg	ggc	aac	ccc	aaa	cag	cct	aca	aat	cct	ttc	ctg	gaa	atg	1949	
Lys	Lys	Leu	Gly	Asn	Pro	Lys	Gln	Pro	Thr	Asn	Pro	Phe	Leu	Glu	Met		
585					590					595					600		
atc	aag	ttt	ctc	ttg	gag	agg	ata	gca	cct	gtg	cac	ata	gat	acc	gaa	1997	
Ile	Lys	Phe	Leu	Leu	Glu	Arg	Ile	Ala	Pro	Val	His	Ile	Asp	Thr	Glu		
				605				610						615			
tct	atc	agt	gct	ctt	att	aaa	caa	gtg	aac	aaa	tca	ata	gat	gga	aca	2045	
Ser	Ile	Ser	Ala	Leu	Ile	Lys	Gln	Val	Asn	Lys	Ser	Ile	Asp	Gly	Thr		
			620					625					630				
gca	gat	gat	gaa	gat	gag	ggt	gtt	cca	act	gat	caa	gcc	atc	aga	gca	2093	

Ala Asp Asp Glu Asp Glu Gly Val Pro Thr Asp Gln Ala Ile Arg Ala	
635 640 645	
ggc ctt gaa ctg ctt aag gta ctc tca ttt aca cat ccc atc tca ttt	2141
Gly Leu Glu Leu Leu Lys Val Leu Ser Phe Thr His Pro Ile Ser Phe	
650 655 660	
cat tct gct gaa aca ttt gaa tca tta ctg gct tgt ctg aaa atg gat	2189
His Ser Ala Glu Thr Phe Glu Ser Leu Leu Ala Cys Leu Lys Met Asp	
665 670 675 680	
gat gaa aaa gta gca gaa gct gca cta caa att ttc aaa aac aca gga	2237
Asp Glu Lys Val Ala Glu Ala Ala Leu Gln Ile Phe Lys Asn Thr Gly	
685 690 695	
agc aaa att gaa gag gat ttt cca cac atc aga tca gcc ttg ctt cct	2285
Ser Lys Ile Glu Glu Asp Phe Pro His Ile Arg Ser Ala Leu Leu Pro	
700 705 710	
gtt tta cat cac aaa tct aaa aaa gga ccc ccc cgt caa gcc aaa tat	2333
Val Leu His His Lys Ser Lys Lys Gly Pro Pro Arg Gln Ala Lys Tyr	
715 720 725	
gcc att cat tgt atc cat gcg ata ttt tct agt aaa gag acc cag ttt	2381
Ala Ile His Cys Ile His Ala Ile Phe Ser Ser Lys Glu Thr Gln Phe	
730 735 740	
gca cag ata ttt gag cct ctg cat aag agc cta gat cca agc aac ctg	2429
Ala Gln Ile Phe Glu Pro Leu His Lys Ser Leu Asp Pro Ser Asn Leu	
745 750 755 760	
gaa cat ctc ata aca cca ttg gtt act att ggt cat att gct ctc ctt	2477
Glu His Leu Ile Thr Pro Leu Val Thr Ile Gly His Ile Ala Leu Leu	
765 770 775	
gca cct gat caa ttt gct gct cct tgg aaa tct tgg gta gct act ttc	2525
Ala Pro Asp Gln Phe Ala Ala Pro Trp Lys Ser Trp Val Ala Thr Phe	
780 785 790	
att gtg aaa gat ctt ctc atg aat gat cgg ctt cca ggg aaa aag aca	2573
Ile Val Lys Asp Leu Leu Met Asn Asp Arg Leu Pro Gly Lys Lys Thr	
795 800 805	
act aaa ctt tgg gtt cca gat gaa gaa gta tct cct gag aca atg gtc	2621
Thr Lys Leu Trp Val Pro Asp Glu Glu Val Ser Pro Glu Thr Met Val	
810 815 820	
aaa att cag gct att aaa atg atg gtt cga tgg cta ctt gga atg aaa	2669
Lys Ile Gln Ala Ile Lys Met Met Val Arg Trp Leu Leu Gly Met Lys	
825 830 835 840	
aat aat cac agt aaa tca gga act tct acc tta aga ttg cta aca aca	2717
Asn Asn His Ser Lys Ser Gly Thr Ser Thr Leu Arg Leu Leu Thr Thr	
845 850 855	
ata ttg cat agt gat gga gac ttg aca gaa cag ggg aaa att agt aaa	2765
Ile Leu His Ser Asp Gly Asp Leu Thr Glu Gln Gly Lys Ile Ser Lys	
860 865 870	
cca gat atg tca cgt ctg aga ctt gct gct ggg agt gct att gtg aag	2813
Pro Asp Met Ser Arg Leu Arg Leu Ala Ala Gly Ser Ala Ile Val Lys	
875 880 885	
ctg gca caa gaa ccc tgt tac cat gaa atc atc aca tta gaa caa tat	2861



Ser Gln Thr Lys Ser Ser Arg Met Glu Thr Val Ser Asn Ala Ser Ser 1145 1150 1155 1160  
 agc tca aat cca agc tct cct gga aga ata aag ggg agg ctt gat agt 3677  
 Ser Ser Asn Pro Ser Ser Pro Gly Arg Ile Lys Gly Arg Leu Asp Ser 1165 1170 1175  
 tct gaa atg gat cac agt gaa aat gaa gat tac aca atg tct tca cct 3725  
 Ser Glu Met Asp His Ser Glu Asn Glu Asp Tyr Thr Met Ser Ser Pro 1180 1185 1190  
 ttg ccg ggg aaa aaa agt gac aag aga gac gac tct gat ctt gta agg 3773  
 Leu Pro Gly Lys Lys Ser Asp Lys Arg Asp Asp Ser Asp Leu Val Arg 1195 1200 1205  
 tct gaa ttg gag aag cct aga ggc agg aaa aaa acg ccc gtc aca gaa 3821  
 Ser Glu Leu Glu Lys Pro Arg Gly Arg Lys Lys Thr Pro Val Thr Glu 1210 1215 1220  
 cag gag gag aaa tta ggt atg gat gac ttg act aag ttg gta cag gaa 3869  
 Gln Glu Glu Lys Leu Gly Met Asp Asp Leu Thr Lys Leu Val Gln Glu 1225 1230 1235 1240  
 cag aaa cct aaa ggc agt cag cga agt cgg aaa aga ggc cat acg gct 3917  
 Gln Lys Pro Lys Gly Ser Gln Arg Ser Arg Lys Arg Gly His Thr Ala 1245 1250 1255  
 tca gaa tct gat gaa cag cag tgg cct gag gaa aag agg ctc aaa gaa 3965  
 Ser Glu Ser Asp Glu Gln Gln Trp Pro Glu Glu Lys Arg Leu Lys Glu 1260 1265 1270  
 gat ata tta gaa aat gaa gat gaa cag aat agt ccg cca aaa aag ggt 4013  
 Asp Ile Leu Glu Asn Glu Asp Glu Gln Asn Ser Pro Pro Lys Lys Gly 1275 1280 1285  
 aaa aga ggc cga cca cca aaa cct ctt ggt gga ggt aca cca aaa gaa 4061  
 Lys Arg Gly Arg Pro Pro Lys Pro Leu Gly Gly Thr Pro Lys Glu 1290 1295 1300  
 gag cca aca atg aaa act tct aaa aaa gga agc aaa aaa aaa tct gga 4109  
 Glu Pro Thr Met Lys Thr Ser Lys Lys Gly Ser Lys Lys Lys Ser Gly 1305 1310 1315 1320  
 cct cca gca cca gag gag gag gaa gaa gaa gaa aga caa agt gga aat 4157  
 Pro Pro Ala Pro Glu Glu Glu Glu Glu Glu Glu Arg Gln Ser Gly Asn 1325 1330 1335  
 acg gaa cag aag tcc aaa agc aaa cag cac cga gtg tca agg aga gca 4205  
 Thr Glu Gln Lys Ser Lys Ser Lys Gln His Arg Val Ser Arg Arg Ala 1340 1345 1350  
 cag cag aga gca gaa tct cct gaa tct agt gca att gaa tcc aca cag 4253  
 Gln Gln Arg Ala Glu Ser Pro Glu Ser Ser Ala Ile Glu Ser Thr Gln 1355 1360 1365  
 tcc aca cca cag aaa gga cga gga aga cca tca aaa acg cca tca cca 4301  
 Ser Thr Pro Gln Lys Gly Arg Gly Arg Pro Ser Lys Thr Pro Ser Pro 1370 1375 1380  
 tca caa cca aaa aaa aat gtg taagttgtaa atattacatt tcaaaccaat 4352  
 Ser Gln Pro Lys Lys Asn Val 1385 1390  
 ttcaaattat ttgcaaaag ttccataaatt tgtaaacata catattgctg tattttaaatt 4412

ccatatat t agccccatta cactaggtac ggcggcgaag tgctaaaagg gaacggcgat 4472  
gaacaaatgt aattaataac tttctctgtg aaagctttgg aaaaatcttt tttttttttt 4532  
tttttttttg gtcaagcttg aggctgaata aagcctttga tgcacaaaat gggactgctg 4592  
aagagtggac agttggacct tactttggtg accccatata tttgtgggtca catgctttag 4652  
ccatacacat ggtaacattg actatggagt cttgtgaaag tgtaatgtgc gatggctatg 4712  
tagacataaa gaagaaactt gtaaataatct tttttctttt ttttaatgtt tctgatttct 4772  
gaagtgcctg tatagctttt atctgcggct ttaaactgac agtaccgcac tgttttattgg 4832  
atctattgat ttgaaaagaa tttgttagga tagatcttaa gcagtaatct gtcagtgttt 4892  
gtatttgtat tttctgcaat tttactgtga aaaaaaat tttttcaaca attgggtgtca 4952  
ttttcttgat gtcactat tttggagagt taaatggtct cttccctttg tgtatcttac 5012  
ctagtgttta ctctgggca cccttaatct tcagaggtgc taaattgtct gccattacac 5072  
cagaaggatg cctctgatag gaggacaacc atgcaaattg tgaaatagtc ctgaagttct 5132  
tggattactt tacacctcag tattgatttg tcccagaatt ttctggcctt tcatggcaat 5192  
gaaaatttta agaagaaaga tttaaagtat ttttaatttta aagagtgtgt tataaaataa 5252  
tgtactgaat tctttatccc attttatcat cctttcagtt tttattaatc tactgtatca 5312  
ataaaattct gtaatttgaa tgagtaaaaa aaaaaaaaaa aaa 5355

<210> 5  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Sequence

<400> 5  
ctawwagscc csgcscaw

18